

SEQUENCE LISTING

<110> Valenzuela et al.

<120> DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS

<130> REG132-B1

<140> Not Yet Known

<141> Filed Herewith

<150> 09/167,874

<151> 1998-10-07

<150> 08/485,721

<151> 1995-07-06

<150> 08/392,935

<151> 1995-09-22

<150> PCT/US93/08326

<151> 1993-09-02

<150> 07/957,401

<151> 1992-10-06

<150> 07/950,410

<151> 1992-09-23

<150> 07/939,954

<151> 1992-09-03

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 699

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(696)

<400> 1

atg gag cgc tgc ccc agc cta ggg gtc acc ctc tac gcc ctg gtg gtg 48
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
1 5 10 15

gtc ctg ggg ctg cgg gcg aca ccg gcc ggc ggc cag cac tat ctc cac 96

Val	Leu	Gly	Leu	Arg	Ala	Thr	Pro	Ala	Gly	Gly	Gln	His	Tyr	Leu	His	
20							25							30		
atc cgc ccg gca ccc agc gac aac ctg ccc ctg gtg gac ctc atc gaa															144	
Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu	
35							40							45		
cac cca gac cct atc ttt gac ccc aag gaa aag gat ctg aac gag acg															192	
His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr	
50							55							60		
ctg ctg cgc tcg ctg ctc ggg ggc cac tac gac cca ggc ttc atg gcc															240	
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala	
65							70							75		
acc tcg ccc ccc gag gac cgg ccc ggc ggg ggg ggg ggt gca gct ggg															288	
Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Ala	Ala	Gly		
85							90							95		
ggc gcg gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccc															336	
Gly	Ala	Glu	Asp	Leu	Ala	Glu	Leu	Asp	Gln	Leu	Leu	Arg	Gln	Arg	Pro	
100							105							110		
tcg ggg gcc atg ccg agc gag atc aaa ggg cta gag ttc tcc gag ggc															384	
Ser	Gly	Ala	Met	Pro	Ser	Glu	Ile	Lys	Gly	Leu	Glu	Phe	Ser	Glu	Gly	
115							120							125		
ttg gcc cag ggc aag aag cag cgc cta agc aag aag ctg cgg agg aag															432	
Leu	Ala	Gln	Gly	Lys	Lys	Gln	Arg	Leu	Ser	Lys	Lys	Leu	Arg	Arg	Lys	
130							135							140		
tta cag atg tgg ctg tgg tcg cag aca ttc tgc ccc gtg ctg tac gcg															480	
Leu	Gln	Met	Trp	Leu	Trp	Ser	Gln	Thr	Phe	Cys	Pro	Val	Leu	Tyr	Ala	
145							150							155		
tgg aac gac ctg ggc agc cgc ttt tgg cgc cgc tac gtg aag gtg ggc															528	
Trp	Asn	Asp	Leu	Gly	Ser	Arg	Phe	Trp	Pro	Arg	Tyr	Val	Lys	Val	Gly	
165							170							175		
agc tgc ttc agt aag cgc tcg tgc tcc gtg ccc gag ggc atg gtg tgc															576	
Ser	Cys	Phe	Ser	Lys	Arg	Ser	Cys	Ser	Val	Pro	Glu	Gly	Met	Val	Cys	
180							185							190		
aag ccg tcc aag tcc gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag															624	
Lys	Pro	Ser	Lys	Ser	Val	His	Leu	Thr	Val	Leu	Arg	Trp	Arg	Cys	Gln	
195							200							205		
cgg cgc ggg ggc cag cgc tgc ggc tgg att ccc atc cag tac ccc atc															6.72	

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
210 215 220

att tcc gag tgc aag tgc tcg tgc tag 699
Ile Ser Glu Cys Lys Cys Ser Cys
225 230

<210> 2
<211> 232
<212> PRT
<213> Homo sapiens

<400> 2
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val
1 5 10 15

Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
20 25 30

Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Ala Ala Gly
85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys

180

185

190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
195 200 205

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
210 215 220

Ile Ser Glu Cys Lys Cys Ser Cys
225 230

<210> 3

<211> 14

<212> PRT

<213> frog and mouse

<400> 3

Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr
1 5 10

<210> 4

<211> 12

<212> PRT

<213> frog and mouse

<400> 4

Arg Phe Trp Pro Arg Tyr Val Lys Val Gly Ser Cys
1 5 10

<210> 5

<211> 14

<212> PRT

<213> frog and mouse

<400> 5

Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys Lys
1 5 10

<210> 6

<211> 8

<212> PRT

<213> frog and mouse

<400> 6

Leu Arg Trp Arg Cys Gln Arg Arg
1 5

<210> 7
<211> 8
<212> PRT
<213> frog and mouse

<400> 7
Ile Ser Glu Cys Lys Cys Ser Cys
1 5

<210> 8
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 8
gactcgagtc gacatcgca atgtggctgt ggtcac

36

<210> 9
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 9
ccaaagttctt agaattcgca ggaacactta cactcg

37

<210> 10
<211> 1180
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (421)..(1116)

<220>

<221> modified_base
<222> (16)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (235)
<223> n=a, c, g, or t

<400> 10

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gaatttgtgag cggtataacaa tttcacacag gaaacagcta tgaccatgtat tacgccaagc 120

tcgaaattaa ccctcaactaa agggaaacaaa agctggagct ccaccgcggg ggcggccgccc 180

tcccaagta gagcggcggg gggaaattgc gaccaactcg tgcgctgtt ctgcncggcg 240

gcgggagccg gcgctgcgcg aacggctctc ctgcagctc atgctgcctg ccctgcgcct 300

gctcagcctc gggtgagcca ctcggagg gaccggggag cgccggcagcg ccgcggactc 360

ggcgtgtctc ctcggggga cgccggacga agaggcagcc ccggggcgcg cgccggaggc 420

atg gag cgc tgc ccc agc ctg ggg gtc acc ctc tac gcc ctg gtg gtg 468
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val

1

5

10

15

gtc ctg ggg ctg cgg gca gca cca gcc ggc cag cac tat cta cac 516
Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His

20

25

30

atc cgc cca gca ccc agc gac aac ctg ccc ttg gtg gac ctc atc gaa 564
Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu

35

40

45

cat cca gac cct atc ttt gac cct aag gag aag gat ctg aac gag acg 612
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr

50

55

60

ctg ctg cgc tcg ctc ggg ggc cac tac gac ccg ggc ttt atg gcc 660
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala

65

70

75

80

act tcg ccc cca gag gac cga ccc gga ggg ggc ggg gga ccg gct gga 708
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Pro Ala Gly

85

90

95

ggt gcc gag gac ctg gcg gag ctg gac cag ctg ctg cgg cag cgg ccg				756
Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro				
100	105	110		
tcg ggg gcc atg ccg agc gag atc aaa ggg ctg gag ttc tcc gag ggc				804
Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly				
115	120	125		
ttg gcc caa ggc aag aaa cag cgc ctg agc aag aag ctg agg agg aag				852
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys				
130	135	140		
tta cag atg tgg ctg tgg tca cag acc ttc tgc ccg gtg ctg tac gcg				900
Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala				
145	150	155	160	
tgg aat gac cta ggc agc cgc ttt tgg cca cgc tac gtg aag gtg ggc				948
Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly				
165	170	175		
agc tgc ttc agc aag cgc tcc tgc tct gtg ccc gag ggc atg gtg tgt				996
Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys				
180	185	190		
aag cca tcc aag tct gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag				1044
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln				
195	200	205		
cgg cgc ggg ggt cag cgc tgc ggc tgg att ccc atc cag tac ccc atc				1092
Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile				
210	215	220		
att tcc gag tgt aag tgt tcc tgc tagaactcg gggggggccc tgcccgcc 1146				
Ile Ser Glu Cys Lys Cys Ser Cys				
225	230			
cagacacttg atggatcccc cgggctgaga tttt				1180
<210> 11				
<211> 232				
<212> PRT				
<213> mouse				
<400> 11				
Met Glu Arg Cys Pro Ser Leu Gly Val Thr Leu Tyr Ala Leu Val Val				
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Val Leu Gly Leu Arg Ala Ala Pro Ala Gly Gly Gln His Tyr Leu His
20 25 30

Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
35 40 45

His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
50 55 60

Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
65 70 75 80

Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Pro Ala Gly
85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
130 135 140

Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
145 150 155 160

Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys
180 185 190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
195 200 205

Arg Arg Gly Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
210 215 220

Ile Ser Glu Cys Lys Cys Ser Cys
225 230

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> modified_base
<222> (6)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (15)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (18)
<223> n=a, c, g, or t

<400> 12
caracn ttyt gyc cngtn

18

<210> 13
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

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<222> (9)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (12)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (18)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (24)

<223> n=a, c, g, or t

<400> 13

ttytggccnm gntaygtnaa rgtngg

26

<210> 14

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> modified_base

<222> (3)

<223> n=a, c, g, or t

<220>

<221> modified_base

<222> (9)

<223> n=a, c, g, or t

<220>

<221> modified_base

<222> (15)

<223> n=a, c, g, or t

<400> 14

ccngarggna tggtntg

17

<210> 15

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> modified_base

<222> (3)

<223> n=a, c, g, or t

<400> 15

canswrcayt trcaytc

17

<210> 16
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> modified_base
<222> (3)
<223> n=a, c, g, or t

<220>
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<222> (9)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (15)
<223> n=a, c, g, or t

<400> 16
canaccatnc cytcngg

17

<210> 17
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> modified_base
<222> (3)
<223> n=a, c, g, or t

<220>
<221> modified_base
<222> (12)
<223> n=a, c, g, or t

<400> 17

cknckytgrc anckcca

17

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 18
cagatgtggc tgtggtca

18

<210> 19
<211> 6
<212> PRT
<213> mouse

<400> 19
Gln Met Trp Leu Trp Ser
1 5

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<400> 20
gcaggaacac ttacactc

18

<210> 21
<211> 6
<212> PRT
<213> mouse

<400> 21
Glu Cys Lys Cys Ser Cys
1 5

<210> 22

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<400> 22
garggnatgg tntgyaarcc

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